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SEQUENCE LISTING

TECH CENTER 1600/2900

E3
<110> De Sauvage, Frederic J.
Klein, Richard D.
Rosenthal, Arnon
Phillips, Heidi S.

<120> GFRALPHA3 AND ITS USES

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<140> 09/272,835

<141> 1999-03-19

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<213> Mus musculus

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ccttctgttc tgatggtgat tagcggtca cctccagcgc ttcttcctgt tccccaggac 300
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<213> Mus musculus

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ccacttgag caggaaactc ccttgccaca gagaacaggt ttgtgaacag ctgtaccag 180
gccagaaaga aatgcgaggc taatcccgtg tgcaaggctg cctaccagca cctgggctcc 240
tgcacctcca gttaagcagg ccgctgccct tagaggagtc tgccatgtct gcagactgcc 300
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<210> 3

<211> 498

<212> DNA

<213> Mus musculus

E3

<400> 3

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agtgggactc cgacaaatgt gaagaacagc tggaagagac catcaaaaac tgcctgtctg 180
cagcagagga caagaagctt aaatccgtcg ccttcccacc gttcccaggt ggcagaaact 240
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<210> 4

<211> 1935

<212> DNA

<213> Mus musculus

<400> 4

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<210> 5

<211> 397

<212> PRT

<213> Mus musculus

E3

<400> 5

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			20					25					30		
Thr	Glu	Asn	Arg	Phe	Val	Asn	Ser	Cys	Thr	Gln	Ala	Arg	Lys	Lys	Cys
		35					40					45			
Glu	Ala	Asn	Pro	Ala	Cys	Lys	Ala	Ala	Tyr	Gln	His	Leu	Gly	Ser	Cys
	50					55					60				
Thr	Ser	Ser	Leu	Ser	Arg	Pro	Leu	Pro	Leu	Glu	Ser	Ala	Met	Ser	
65					70					75				80	
Ala	Asp	Cys	Leu	Glu	Ala	Ala	Glu	Gln	Leu	Arg	Asn	Ser	Ser	Leu	Ile
			85						90					95	
Asp	Cys	Arg	Cys	His	Arg	Arg	Met	Lys	His	Gln	Ala	Thr	Cys	Leu	Asp
			100					105					110		
Ile	Tyr	Trp	Thr	Val	His	Pro	Ala	Arg	Ser	Leu	Gly	Asp	Tyr	Glu	Leu
	115						120					125			
Asp	Val	Ser	Pro	Tyr	Glu	Asp	Thr	Val	Thr	Ser	Lys	Pro	Trp	Lys	Met
	130					135					140				
Asn	Leu	Ser	Lys	Leu	Asn	Met	Leu	Lys	Pro	Asp	Ser	Asp	Leu	Cys	Leu
145					150					155					160
Lys	Phe	Ala	Met	Leu	Cys	Thr	Leu	His	Asp	Lys	Cys	Asp	Arg	Leu	Arg
			165						170					175	
Lys	Ala	Tyr	Gly	Glu	Ala	Cys	Ser	Gly	Ile	Arg	Cys	Gln	Arg	His	Leu
			180					185					190		
Cys	Leu	Ala	Gln	Leu	Arg	Ser	Phe	Phe	Glu	Lys	Ala	Ala	Glu	Ser	His
	195						200					205			
Ala	Gln	Gly	Leu	Leu	Leu	Cys	Pro	Cys	Ala	Pro	Glu	Asp	Ala	Gly	Cys
	210					215					220				
Gly	Glu	Arg	Arg	Arg	Asn	Thr	Ile	Ala	Pro	Ser	Cys	Ala	Leu	Pro	Ser
225					230					235					240
Val	Thr	Pro	Asn	Cys	Leu	Asp	Leu	Arg	Ser	Phe	Cys	Arg	Ala	Asp	Pro
			245						250					255	
Leu	Cys	Arg	Ser	Arg	Leu	Met	Asp	Phe	Gln	Thr	His	Cys	His	Pro	Met
			260					265					270		
Asp	Ile	Leu	Gly	Thr	Cys	Ala	Thr	Glu	Gln	Ser	Arg	Cys	Leu	Arg	Ala
	275						280					285			
Tyr	Leu	Gly	Leu	Ile	Gly	Thr	Ala	Met	Thr	Pro	Asn	Phe	Ile	Ser	Lys
	290					295					300				
Val	Asn	Thr	Thr	Val	Ala	Leu	Ser	Cys	Thr	Cys	Arg	Gly	Ser	Gly	Asn
305					310					315					320
Leu	Gln	Asp	Glu	Cys	Glu	Gln	Leu	Glu	Arg	Ser	Phe	Ser	Gln	Asn	Pro
			325						330					335	
Cys	Leu	Val	Glu	Ala	Ile	Ala	Ala	Lys	Met	Arg	Phe	His	Arg	Gln	Leu
			340					345					350		
Phe	Ser	Gln	Asp	Trp	Ala	Asp	Ser	Thr	Phe	Ser	Val	Val	Gln	Gln	Gln
	355						360					365			
Asn	Ser	Asn	Pro	Ala	Leu	Arg	Leu	Gln	Pro	Arg	Leu	Pro	Ile	Leu	Ser
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Phe	Ser	Ile	Leu	Pro	Leu	Ile	Leu	Leu	Gln	Thr	Leu	Trp			
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<210> 6

<211> 460

<212> PRT

<213> Homo sapiens

E3

<400> 6

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Ser	Asp	Gln	Cys	Leu	Lys	Glu	Gln	Ser	Cys	Ser	Thr	Lys	Tyr	Arg	Thr	35	40	45	
Leu	Arg	Gln	Cys	Val	Ala	Gly	Lys	Glu	Thr	Asn	Phe	Ser	Leu	Ala	Ser	50	55	60	
Gly	Leu	Glu	Ala	Lys	Asp	Glu	Cys	Arg	Ser	Ala	Met	Glu	Ala	Leu	Lys	65	70	75	80
Gln	Lys	Ser	Leu	Tyr	Asn	Cys	Arg	Cys	Lys	Arg	Gly	Met	Lys	Lys	Glu	85	90	95	
Lys	Asn	Cys	Leu	Arg	Ile	Tyr	Trp	Ser	Met	Tyr	Gln	Ser	Leu	Gln	Gly	100	105	110	
Asn	Asp	Leu	Leu	Glu	Asp	Ser	Pro	Tyr	Glu	Pro	Val	Asn	Ser	Arg	Leu	115	120	125	
Ser	Asp	Ile	Phe	Arg	Val	Val	Pro	Phe	Ile	Ser	Val	Glu	His	Ile	Pro	130	135	140	
Lys	Gly	Asn	Asn	Cys	Leu	Asp	Ala	Ala	Lys	Ala	Cys	Asn	Leu	Asp	Asp	145	150	155	160
Ile	Cys	Lys	Lys	Tyr	Arg	Ser	Ala	Tyr	Ile	Thr	Pro	Cys	Thr	Thr	Ser	165	170	175	
Val	Ser	Asn	Asp	Val	Cys	Asn	Arg	Arg	Lys	Cys	His	Lys	Ala	Leu	Arg	180	185	190	
Gln	Phe	Phe	Asp	Lys	Val	Pro	Ala	Lys	His	Ser	Tyr	Gly	Met	Leu	Phe	195	200	205	
Cys	Ser	Cys	Arg	Asp	Ile	Ala	Cys	Thr	Glu	Arg	Arg	Arg	Gln	Thr	Ile	210	215	220	
Val	Pro	Val	Cys	Ser	Tyr	Glu	Glu	Arg	Glu	Lys	Pro	Asn	Cys	Leu	Asn	225	230	235	240
Leu	Gln	Asp	Ser	Cys	Lys	Thr	Asn	Tyr	Ile	Cys	Arg	Ser	Arg	Leu	Ala	245	250	255	
Asp	Phe	Phe	Thr	Asn	Cys	Gln	Pro	Glu	Ser	Arg	Ser	Val	Ser	Ser	Cys	260	265	270	
Leu	Lys	Glu	Asn	Tyr	Ala	Asp	Cys	Leu	Leu	Ala	Tyr	Ser	Gly	Leu	Ile	275	280	285	
Gly	Thr	Val	Met	Thr	Pro	Asn	Tyr	Ile	Asp	Ser	Ser	Ser	Leu	Ser	Val	290	295	300	
Ala	Pro	Trp	Cys	Asp	Cys	Ser	Asn	Ser	Gly	Asn	Asp	Leu	Glu	Glu	Cys	305	310	315	320
Leu	Lys	Phe	Leu	Asn	Phe	Phe	Lys	Asp	Asn	Thr	Cys	Leu	Lys	Asn	Ala	325	330	335	
Ile	Gln	Ala	Phe	Gly	Asn	Gly	Ser	Asp	Val	Thr	Val	Trp	Gln	Pro	Ala	340	345	350	
Phe	Pro	Val	Gln	Thr	Thr	Thr	Ala	Thr	Thr	Thr	Thr	Ala	Leu	Arg	Val	355	360	365	
Lys	Asn	Lys	Pro	Leu	Gly	Pro	Ala	Gly	Ser	Glu	Asn	Glu	Ile	Pro	Thr	370	375	380	
His	Val	Leu	Pro	Pro	Cys	Ala	Asn	Leu	Gln	Ala	Gln	Lys	Leu	Lys	Ser	385	390	395	400
Asn	Val	Ser	Gly	Asn	Thr	His	Leu	Cys	Ile	Ser	Asn	Gly	Asn	Tyr	Glu	405	410	415	
Lys	Glu	Gly	Leu	Gly	Ala	Ser	Ser	His	Ile	Thr	Thr	Lys	Ser	Met	Ala	420	425	430	
Ala	Pro	Pro	Ser	Cys	Gly	Leu	Ser	Pro	Leu	Leu	Val	Leu	Val	Val	Thr				

E3

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Ala	Leu	Ser	Thr	Leu	Leu	Ser	Leu	Thr	Glu	Thr	Ser	
	450					455					460	

<210> 7
 <211> 464
 <212> PRT
 <213> Homo sapiens

<400> 7

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			20					25					30		
Gly	Trp	Arg	Pro	Pro	Val	Asp	Cys	Val	Arg	Ala	Asn	Glu	Leu	Cys	Ala
			35				40					45			
Ala	Glu	Ser	Asn	Cys	Ser	Ser	Arg	Tyr	Arg	Thr	Leu	Arg	Gln	Cys	Leu
	50					55					60				
Ala	Gly	Arg	Asp	Arg	Asn	Thr	Met	Leu	Ala	Asn	Lys	Glu	Cys	Gln	Ala
65					70					75					80
Ala	Leu	Glu	Val	Leu	Gln	Glu	Ser	Pro	Leu	Tyr	Asp	Cys	Arg	Cys	Lys
				85					90					95	
Arg	Gly	Met	Lys	Lys	Glu	Leu	Gln	Cys	Leu	Gln	Ile	Tyr	Trp	Ser	Ile
			100					105					110		
His	Leu	Gly	Leu	Thr	Glu	Gly	Glu	Glu	Phe	Tyr	Glu	Ala	Ser	Pro	Tyr
	115						120					125			
Glu	Pro	Val	Thr	Ser	Arg	Leu	Ser	Asp	Ile	Phe	Arg	Leu	Ala	Ser	Ile
	130					135					140				
Phe	Ser	Gly	Thr	Gly	Ala	Asp	Pro	Val	Val	Ser	Ala	Lys	Ser	Asn	His
145					150					155					160
Cys	Leu	Asp	Ala	Ala	Lys	Ala	Cys	Asn	Leu	Asn	Asp	Asn	Cys	Lys	Lys
				165					170					175	
Leu	Arg	Ser	Ser	Tyr	Ile	Ser	Ile	Cys	Asn	Arg	Glu	Ile	Ser	Pro	Thr
			180					185					190		
Glu	Arg	Cys	Asn	Arg	Arg	Lys	Cys	His	Lys	Ala	Leu	Arg	Gln	Phe	Phe
		195					200					205			
Asp	Arg	Val	Pro	Ser	Glu	Tyr	Thr	Tyr	Arg	Met	Leu	Phe	Cys	Ser	Cys
	210					215					220				
Gln	Asp	Gln	Ala	Cys	Ala	Glu	Arg	Arg	Arg	Gln	Thr	Ile	Leu	Pro	Ser
225					230					235					240
Cys	Ser	Tyr	Glu	Asp	Lys	Glu	Lys	Pro	Asn	Cys	Leu	Asp	Leu	Arg	Gly
				245					250					255	
Val	Cys	Arg	Thr	Asp	His	Leu	Cys	Arg	Ser	Arg	Leu	Ala	Asp	Phe	His
			260					265					270		
Ala	Asn	Cys	Arg	Ala	Ser	Tyr	Gln	Thr	Val	Thr	Ser	Cys	Pro	Ala	Asp
		275					280					285			
Asn	Tyr	Gln	Ala	Cys	Leu	Gly	Ser	Tyr	Ala	Gly	Met	Ile	Gly	Phe	Asp
	290					295					300				
Met	Thr	Pro	Asn	Tyr	Val	Asp	Ser	Ser	Pro	Thr	Gly	Ile	Val	Val	Ser
305					310					315					320
Pro	Trp	Cys	Ser	Cys	Arg	Gly	Ser	Gly	Asn	Met	Glu	Glu	Glu	Cys	Glu
				325					330					335	
Lys	Phe	Leu	Arg	Asp	Phe	Thr	Glu	Asn	Pro	Cys	Leu	Arg	Asn	Ala	Ile
			340				345						350		
Gln	Ala	Phe	Gly	Asn	Gly	Thr	Asp	Val	Asn	Val	Ser	Pro	Lys	Gly	Pro
		355					360					365			

E3

Ser	Phe	Gln	Ala	Thr	Gln	Ala	Pro	Arg	Val	Glu	Lys	Thr	Pro	Ser	Leu
	370					375					380				
Pro	Asp	Asp	Leu	Ser	Asp	Ser	Thr	Ser	Leu	Gly	Thr	Ser	Val	Ile	Thr
385					390					395					400
Thr	Cys	Thr	Ser	Val	Gln	Glu	Gln	Gly	Leu	Lys	Ala	Asn	Asn	Ser	Lys
				405					410						415
Glu	Leu	Ser	Met	Cys	Phe	Thr	Glu	Leu	Thr	Thr	Asn	Ile	Ile	Pro	Gly
			420					425					430		
Ser	Asn	Lys	Val	Ile	Lys	Pro	Asn	Ser	Gly	Pro	Ser	Arg	Ala	Arg	Pro
	435						440					445			
Ser	Ala	Ala	Leu	Thr	Val	Leu	Ser	Val	Leu	Met	Leu	Lys	Leu	Ala	Leu
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<210> 8

<211> 468

<212> PRT

<213> Rattus norvegicus

<400> 8

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Met	Ser	Ala	Glu	Val	Ser	Gly	Gly	Asp	Arg	Leu	Asp	Cys	Val	Lys	Ala
			20					25					30		
Ser	Asp	Gln	Cys	Leu	Lys	Glu	Gln	Ser	Cys	Ser	Thr	Lys	Tyr	Arg	Thr
	35						40					45			
Leu	Arg	Gln	Cys	Val	Ala	Gly	Lys	Glu	Thr	Asn	Phe	Ser	Leu	Thr	Ser
	50					55				60					
Gly	Leu	Glu	Ala	Lys	Asp	Glu	Cys	Arg	Ser	Ala	Met	Glu	Ala	Leu	Lys
65				70					75						80
Gln	Lys	Ser	Leu	Tyr	Asn	Cys	Arg	Cys	Lys	Arg	Gly	Met	Lys	Lys	Glu
			85						90					95	
Lys	Asn	Cys	Leu	Arg	Ile	Tyr	Trp	Ser	Met	Tyr	Gln	Ser	Leu	Gln	Gly
			100					105					110		
Asn	Asp	Leu	Leu	Glu	Asp	Ser	Pro	Tyr	Glu	Pro	Val	Asn	Ser	Arg	Leu
	115						120					125			
Ser	Asp	Ile	Phe	Arg	Ala	Val	Pro	Phe	Ile	Ser	Asp	Val	Phe	Gln	Gln
	130					135					140				
Val	Glu	His	Ile	Ser	Lys	Gly	Asn	Asn	Cys	Leu	Asp	Ala	Ala	Lys	Ala
145					150					155					160
Cys	Asn	Leu	Asp	Asp	Thr	Cys	Lys	Lys	Tyr	Arg	Ser	Ala	Tyr	Ile	Thr
			165						170					175	
Pro	Cys	Thr	Thr	Ser	Met	Ser	Asn	Glu	Val	Cys	Asn	Arg	Arg	Lys	Cys
			180					185					190		
His	Lys	Ala	Leu	Arg	Gln	Phe	Phe	Asp	Lys	Val	Pro	Ala	Lys	His	Ser
	195						200					205			
Tyr	Gly	Met	Leu	Phe	Cys	Ser	Cys	Arg	Asp	Ile	Ala	Cys	Thr	Glu	Arg
	210					215					220				
Arg	Arg	Gln	Thr	Ile	Val	Pro	Val	Cys	Ser	Tyr	Glu	Glu	Arg	Glu	Arg
225					230					235					240
Pro	Asn	Cys	Leu	Ser	Leu	Gln	Asp	Ser	Cys	Lys	Thr	Asn	Tyr	Ile	Cys
			245						250					255	
Arg	Ser	Arg	Leu	Ala	Asp	Phe	Phe	Thr	Asn	Cys	Gln	Pro	Glu	Ser	Arg
			260					265					270		
Ser	Val	Ser	Asn	Cys	Leu	Lys	Glu	Asn	Tyr	Ala	Asp	Cys	Leu	Leu	Ala
	275						280					285			
Tyr	Ser	Gly	Leu	Ile	Gly	Thr	Val	Met	Thr	Pro	Asn	Tyr	Val	Asp	Ser

E3

290		295		300
Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn				
305		310		315
Asp Leu Glu Asp Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr				
	325		330	
Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr				
	340		345	350
Met Trp Gln Pro Ala Pro Pro Val Gln Thr Thr Thr Ala Thr Thr Thr				
	355		360	365
Thr Ala Phe Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu				
	370	375		380
Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala				
385		390		395
Gln Lys Leu Lys Ser Asn Val Ser Gly Ser Thr His Leu Cys Leu Ser				
	405		410	415
Asp Ser Asp Phe Gly Lys Asp Gly Leu Ala Gly Ala Ser Ser His Ile				
	420		425	430
Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Ser Leu Ser Ser Leu				
	435	440		445
Pro Val Leu Met Leu Thr Ala Leu Ala Ala Leu Leu Ser Val Ser Leu				
	450	455		460
Ala Glu Thr Ser				
465				

<210> 9

<211> 464

<212> PRT

<213> Rattus Norvegicus

<400> 9

Met Ile Leu Ala Asn Ala Phe Cys Leu Phe Phe Phe Leu Asp Glu Thr				
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Leu Arg Ser Leu Ala Ser Pro Ser Ser Leu Gln Gly Ser Glu Leu His				
	20		25	30
Gly Trp Arg Pro Gln Val Asp Cys Val Arg Ala Asn Glu Leu Cys Ala				
	35		40	45
Ala Glu Ser Asn Cys Ser Ser Arg Tyr Arg Thr Leu Arg Gln Cys Leu				
	50		55	60
Ala Gly Arg Asp Arg Asn Thr Met Leu Ala Asn Lys Glu Cys Gln Ala				
65		70		75
Ala Leu Glu Val Leu Gln Glu Ser Pro Leu Tyr Asp Cys Arg Cys Lys				
	85		90	95
Arg Gly Met Lys Lys Glu Leu Gln Cys Leu Gln Ile Tyr Trp Ser Ile				
	100		105	110
His Leu Gly Leu Thr Glu Gly Glu Glu Phe Tyr Glu Ala Ser Pro Tyr				
	115		120	125
Glu Pro Val Thr Ser Arg Leu Ser Asp Ile Phe Arg Leu Ala Ser Ile				
	130		135	140
Phe Ser Gly Thr Gly Thr Asp Pro Ala Val Ser Thr Lys Ser Asn His				
145		150		155
Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asn Asp Asn Cys Lys Lys				
	165		170	175
Leu Arg Ser Ser Tyr Ile Ser Ile Cys Asn Arg Glu Ile Ser Pro Thr				
	180		185	190
Glu Arg Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe				
	195		200	205

Asp	Arg	Val	Pro	Ser	Glu	Tyr	Thr	Tyr	Arg	Met	Leu	Phe	Cys	Ser	Cys
210						215					220				
Gln	Asp	Gln	Ala	Cys	Ala	Glu	Arg	Arg	Arg	Gln	Thr	Ile	Leu	Pro	Ser
225					230					235					240
Cys	Ser	Tyr	Glu	Asp	Lys	Glu	Lys	Pro	Asn	Cys	Leu	Asp	Leu	Arg	Ser
				245					250					255	
Leu	Cys	Arg	Thr	Asp	His	Leu	Cys	Arg	Ser	Arg	Leu	Ala	Asp	Phe	His
			260					265					270		
Ala	Asn	Cys	Arg	Ala	Ser	Tyr	Arg	Thr	Ile	Thr	Ser	Cys	Pro	Ala	Asp
		275					280					285			
Asn	Tyr	Gln	Ala	Cys	Leu	Gly	Ser	Tyr	Ala	Gly	Met	Ile	Gly	Phe	Asp
290						295					300				
Met	Thr	Pro	Asn	Tyr	Val	Asp	Ser	Asn	Pro	Thr	Gly	Ile	Val	Val	Ser
305					310					315					320
Pro	Trp	Cys	Asn	Cys	Arg	Gly	Ser	Gly	Asn	Met	Glu	Glu	Glu	Cys	Glu
				325					330					335	
Lys	Phe	Leu	Arg	Asp	Phe	Thr	Glu	Asn	Pro	Cys	Leu	Arg	Asn	Ala	Ile
			340					345					350		
Gln	Ala	Phe	Gly	Asn	Gly	Thr	Asp	Val	Asn	Met	Ser	Pro	Lys	Gly	Pro
		355					360					365			
Ser	Leu	Pro	Ala	Thr	Gln	Ala	Pro	Arg	Val	Glu	Lys	Thr	Pro	Ser	Leu
	370					375				380					
Pro	Asp	Asp	Leu	Ser	Asp	Ser	Thr	Ser	Leu	Gly	Thr	Ser	Val	Ile	Thr
385					390					395					400
Thr	Cys	Thr	Ser	Ile	Gln	Glu	Gln	Gly	Leu	Lys	Ala	Asn	Asn	Ser	Lys
				405					410					415	
Glu	Leu	Ser	Met	Cys	Phe	Thr	Glu	Leu	Thr	Thr	Asn	Ile	Ser	Pro	Gly
		420						425				430			
Ser	Lys	Lys	Val	Ile	Lys	Leu	Asn	Ser	Gly	Ser	Ser	Arg	Ala	Arg	Leu
		435					440					445			
Ser	Ala	Ala	Leu	Thr	Ala	Leu	Pro	Leu	Leu	Met	Leu	Thr	Leu	Ala	Leu
	450					455					460				

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<210> 10
<211> 282
<212> DNA
<213> Homo sapiens
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<220>

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<221> unsure
<222> (0)...(0)
<223> n = A, T, C or G
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cccctgaacc	cgcgaccgct	gccgcccgta	gnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	180	
nnnnnnnnng	ctctcgcagc	cggagacccc	cttcccacag	aaagccgact	catgaacagc	240	
tgtctccagq	ccaqqaqaa	tqccacgqct	qatcccacct	qc		282	

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<210> 11
<211> 20
<212> DNA
<213> Homo sapiens
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E3

<400> 11
gcctctcgca gccggagacc

20

<210> 12
<211> 21
<212> DNA
<213> Homo sapiens

<400> 12
caggtgggat cagcctggca c

21

<210> 13
<211> 41
<212> DNA
<213> Homo sapiens

<400> 13
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41

<210> 14
<211> 1792
<212> DNA
<213> Homo sapiens

<400> 14
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atgaacagct gtctccaggc caggaggaag tgccaggctg atcccacctg cagtgcctgc 180
taccaccacc tggattcctg cactcttagc ataagcacc cactgccttc agaggagcct 240
tcggtccttg ctgactgcct ggaggcagca cagcaactca ggaacagctc tctgataggc 300
tgcatgtgcc accggcgcat gaagaaccag gttgcctgct tggacatcta ttggaccgtt 360
caccgtgccc gcagccttgg taactatgag ctggatgtct cccctatga agacacagt 420
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gcccccaacg accggggctg cggggagcgc cggcgcaaca ccatcgcccc caactgcgcg 720
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cctgccgaac atctgggcat caggagctgg agcctgtggg ccttgcttta ttctattat 1740
tgtcctaaag tctctctggg ctcttgatc atgattaaac ctttgactta ag 1792

<210> 15

E3

<211> 400
 <212> PRT
 <213> Homo Sapiens

<400> 15

Met	Val	Arg	Pro	Leu	Asn	Pro	Arg	Pro	Leu	Pro	Pro	Val	Val	Leu	Met
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Leu	Leu	Leu	Leu	Leu	Pro	Pro	Ser	Pro	Leu	Pro	Leu	Ala	Ala	Gly	Asp
			20					25					30		
Pro	Leu	Pro	Thr	Glu	Ser	Arg	Leu	Met	Asn	Ser	Cys	Leu	Gln	Ala	Arg
		35					40					45			
Arg	Lys	Cys	Gln	Ala	Asp	Pro	Thr	Cys	Ser	Ala	Ala	Tyr	His	His	Leu
	50					55					60				
Asp	Ser	Cys	Thr	Ser	Ser	Ile	Ser	Thr	Pro	Leu	Pro	Ser	Glu	Glu	Pro
65					70					75					80
Ser	Val	Pro	Ala	Asp	Cys	Leu	Glu	Ala	Ala	Gln	Gln	Leu	Arg	Asn	Ser
				85					90					95	
Ser	Leu	Ile	Gly	Cys	Met	Cys	His	Arg	Arg	Met	Lys	Asn	Gln	Val	Ala
			100					105					110		
Cys	Leu	Asp	Ile	Tyr	Trp	Thr	Val	His	Arg	Ala	Arg	Ser	Leu	Gly	Asn
		115					120					125			
Tyr	Glu	Leu	Asp	Val	Ser	Pro	Tyr	Glu	Asp	Thr	Val	Thr	Ser	Lys	Pro
	130					135					140				
Trp	Lys	Met	Asn	Leu	Ser	Lys	Leu	Asn	Met	Leu	Lys	Pro	Asp	Ser	Asp
145				150						155					160
Leu	Cys	Leu	Lys	Phe	Ala	Met	Leu	Cys	Thr	Leu	Asn	Asp	Lys	Cys	Asp
				165					170					175	
Arg	Leu	Arg	Lys	Ala	Tyr	Gly	Glu	Ala	Cys	Ser	Gly	Pro	His	Cys	Gln
			180					185					190		
Arg	His	Val	Cys	Leu	Arg	Gln	Leu	Leu	Thr	Phe	Phe	Glu	Lys	Ala	Ala
		195				200						205			
Glu	Pro	His	Ala	Gln	Gly	Leu	Leu	Leu	Cys	Pro	Cys	Ala	Pro	Asn	Asp
	210					215					220				
Arg	Gly	Cys	Gly	Glu	Arg	Arg	Arg	Asn	Thr	Ile	Ala	Pro	Asn	Cys	Ala
225					230					235					240
Leu	Pro	Pro	Val	Ala	Pro	Asn	Cys	Leu	Glu	Leu	Arg	Arg	Leu	Cys	Phe
				245					250					255	
Ser	Asp	Pro	Leu	Cys	Arg	Ser	Arg	Leu	Val	Asp	Phe	Gln	Thr	His	Cys
		260						265					270		
His	Pro	Met	Asp	Ile	Leu	Gly	Thr	Cys	Ala	Thr	Glu	Gln	Ser	Arg	Cys
		275					280					285			
Leu	Arg	Ala	Tyr	Leu	Gly	Leu	Ile	Gly	Thr	Ala	Met	Thr	Pro	Asn	Phe
	290					295					300				
Val	Ser	Asn	Val	Asn	Thr	Ser	Val	Ala	Leu	Ser	Cys	Thr	Cys	Arg	Gly
305					310					315					320
Ser	Gly	Asn	Leu	Gln	Glu	Glu	Cys	Glu	Met	Leu	Glu	Gly	Phe	Phe	Ser
				325					330					335	
His	Asn	Pro	Cys	Leu	Thr	Glu	Ala	Ile	Ala	Ala	Lys	Met	Arg	Phe	His
			340					345					350		
Ser	Gln	Leu	Phe	Ser	Gln	Asp	Trp	Pro	His	Pro	Thr	Phe	Ala	Val	Met
		355					360					365			
Ala	His	Gln	Asn	Glu	Asn	Pro	Ala	Val	Arg	Pro	Gln	Pro	Trp	Val	Pro
	370					375					380				
Ser	Leu	Phe	Ser	Cys	Thr	Leu	Pro	Leu	Ile	Leu	Leu	Leu	Ser	Leu	Trp
385					390					395					400

E3

<210> 16
 <211> 1837
 <212> DNA
 <213> Homo sapeins

<400> 16

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gcccggcgcc tacagctcgc catggtgcgc cccctgaacc cgcgaccgct gccgcccgtg 180
gtcctgatgt tgctgctgct gctgccgccg tcgccgctgc ctctcgagc cggagacccc 240
cttcccacag aaagccgact catgaacagc tgtctccagg ccaggaggaa gtgccaggct 300
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cggggctgcg gggagcgccg gcgcaacacc atcgcccca actgcgcgct gccgcctgtg 780
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cagtccagat gtctacgagc atacctgggg ctgattggga ctgccatgac cccaactttt 960
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gttagccttt ctctattgca ttccagatta gggttagggt agggaggact ggggtgttctg 1620
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tctctgggct cttggatcat gattaaacct ttgactt 1837

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<210> 17
 <211> 369
 <212> PRT
 <213> Homo sapiens

<400> 17

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Met Val Arg Pro Leu Asn Pro Arg Pro Leu Pro Pro Val Val Leu Met
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Leu Leu Leu Leu Leu Pro Pro Ser Pro Leu Pro Leu Ala Ala Gly Asp
20          25          30
Pro Leu Pro Thr Glu Ser Arg Leu Met Asn Ser Cys Leu Gln Ala Arg
35          40          45
Arg Lys Cys Gln Ala Asp Pro Thr Cys Ser Ala Ala Tyr His His Leu
50          55          60
Asp Ser Cys Thr Ser Ser Ile Ser Thr Pro Leu Pro Ser Glu Glu Pro
65          70          75          80
Ser Val Pro Ala Asp Cys Leu Glu Ala Ala Gln Gln Leu Arg Asn Ser
85          90          95
Ser Leu Ile Gly Cys Met Cys His Arg Arg Met Lys Asn Gln Val Ala

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				85				90				95				
Ser	Leu	Ile	Gly	Cys	Met	Cys	His	Arg	Arg	Met	Lys	Asn	Gln	Val	Ala	
			100							105				110		
Cys	Leu	Asp	Ile	Tyr	Trp	Thr	Val	His	Arg	Ala	Arg	Ser	Leu	Gly	Asn	
			115							120				125		
Tyr	Glu	Leu	Asp	Val	Ser	Pro	Tyr	Glu	Asp	Thr	Val	Thr	Ser	Lys	Pro	
			130							135				140		
Trp	Lys	Met	Asn	Leu	Ser	Lys	Leu	Asn	Met	Leu	Lys	Pro	Asp	Ser	Asp	
145													155			
Leu	Cys	Leu	Lys	Phe	Ala	Met	Leu	Cys	Thr	Leu	Asn	Asp	Lys	Cys	Asp	
			165										170			
Arg	Leu	Arg	Lys	Ala	Tyr	Gly	Glu	Ala	Cys	Ser	Gly	Pro	His	Cys	Gln	
			180										185			
Arg	His	Val	Cys	Leu	Arg	Gln	Leu	Leu	Thr	Phe	Phe	Glu	Lys	Ala	Ala	
			195										200			
Glu	Pro	His	Ala	Gln	Gly	Leu	Leu	Leu	Cys	Pro	Cys	Ala	Pro	Asn	Asp	
			210										215			
Arg	Gly	Cys	Gly	Glu	Arg	Arg	Arg	Asn	Thr	Ile	Ala	Pro	Asn	Cys	Ala	
225													220			
Leu	Pro	Pro	Val	Ala	Pro	Asn	Cys	Leu	Glu	Leu	Arg	Arg	Leu	Cys	Phe	
			230										235			
Ser	Asp	Pro	Leu	Cys	Arg	Ser	Arg	Leu	Val	Asp	Phe	Gln	Thr	His	Cys	
			245										250			
His	Pro	Met	Asp	Ile	Leu	Gly	Thr	Cys	Ala	Thr	Glu	Gln	Ser	Arg	Cys	
			260										265			
Leu	Arg	Ala	Tyr	Leu	Gly	Leu	Ile	Gly	Thr	Ala	Met	Thr	Pro	Asn	Phe	
			275										280			
Val	Ser	Asn	Val	Asn	Thr	Ser	Val	Ala	Leu	Ser	Cys	Thr	Cys	Arg	Gly	
305													295			
Ser	Gly	Asn	Leu	Gln	Glu	Glu	Cys	Glu	Met	Leu	Glu	Gly	Phe	Phe	Ser	
			310										315			
His	Asn	Pro	Cys	Leu	Thr	Glu	Ala	Ile	Ala	Ala	Lys	Met	Arg	Phe	His	
			325										330			
Ser	Gln	Leu	Phe	Ser	Gln	Asp	Trp	Pro	His	Pro	Thr	Phe	Ala	Val	Met	
			340										345			
Ala	His	Gln	Asn	Glu	Asn	Pro	Ala	Val	Arg	Pro	Gln	Pro	Trp	Val	Pro	
			355										360			
Ser	Leu	Phe	Ser	Cys	Thr	Leu	Pro	Leu	Ile	Leu	Leu	Leu	Ser	Leu	Trp	
385													375			
Pro	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	
			390										395			
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	
			405										410			
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	
			420										425			
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	
			435										440			
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	
			450										455			
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	
			465										470			
Gly	Lys	Glu	Tyr	Lys	Cys											

E3

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 545 550 555 560
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 565 570 575
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 580 585 590
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 595 600 605
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 610 615 620
 Ser Pro Gly Lys
 625

<210> 19

<211> 951

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric receptor comprising rat sequence.

<400> 19

Met Gly Gly Thr Ala Ala Arg Leu Gly Ala Val Ile Leu Phe Val Val
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 Ile Val Gly Leu His Gly Val Arg Gly Lys Tyr Ala Leu Ala Asp Ala
 20 25 30
 Ser Leu Lys Met Ala Asp Pro Asn Arg Phe Arg Gly Lys Asp Leu Pro
 35 40 45
 Val Leu Asp Gln Leu Leu Glu Pro Ser Ser Leu Gln Gly Ser Glu Leu
 50 55 60
 His Gly Trp Arg Pro Gln Val Asp Cys Val Arg Ala Asn Glu Leu Cys
 65 70 75 80
 Ala Ala Glu Ser Asn Cys Ser Ser Arg Tyr Arg Thr Leu Arg Gln Cys
 85 90 95
 Leu Ala Gly Arg Asp Arg Asn Thr Met Leu Ala Asn Lys Glu Cys Gln
 100 105 110
 Ala Ala Leu Glu Val Leu Gln Glu Ser Pro Leu Tyr Asp Cys Arg Cys
 115 120 125
 Lys Arg Gly Met Lys Lys Glu Leu Gln Cys Leu Gln Ile Tyr Trp Ser
 130 135 140
 Ile His Leu Gly Leu Thr Glu Gly Glu Glu Phe Tyr Glu Ala Ser Pro
 145 150 155 160
 Tyr Glu Pro Val Thr Ser Arg Leu Ser Asp Ile Phe Arg Leu Ala Ser
 165 170 175
 Ile Phe Ser Gly Thr Gly Thr Asp Pro Ala Val Ser Thr Lys Ser Asn
 180 185 190
 His Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asn Asp Asn Cys Lys
 195 200 205
 Lys Leu Arg Ser Ser Tyr Ile Ser Ile Cys Asn Arg Glu Ile Ser Pro
 210 215 220
 Thr Glu Arg Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe
 225 230 235 240
 Phe Asp Arg Val Pro Ser Glu Tyr Thr Tyr Arg Met Leu Phe Cys Ser
 245 250 255
 Cys Gln Asp Gln Ala Cys Ala Glu Arg Arg Arg Gln Thr Ile Leu Pro
 260 265 270

E3

Ser	Cys	Ser	Tyr	Glu	Asp	Lys	Glu	Lys	Pro	Asn	Cys	Leu	Asp	Leu	Arg	
	275						280					285				
Ser	Leu	Cys	Arg	Thr	Asp	His	Leu	Cys	Arg	Ser	Arg	Leu	Ala	Asp	Phe	
	290					295					300					
His	Ala	Asn	Cys	Arg	Ala	Ser	Tyr	Arg	Thr	Ile	Thr	Ser	Cys	Pro	Ala	
305					310					315					320	
Asp	Asn	Tyr	Gln	Ala	Cys	Leu	Gly	Ser	Tyr	Ala	Gly	Met	Ile	Gly	Phe	
			325						330					335		
Asp	Met	Thr	Pro	Asn	Tyr	Val	Asp	Ser	Asn	Pro	Thr	Gly	Ile	Val	Val	
			340					345					350			
Ser	Pro	Trp	Cys	Asn	Cys	Arg	Gly	Ser	Gly	Asn	Met	Glu	Glu	Glu	Cys	
		355					360					365				
Glu	Lys	Phe	Leu	Arg	Asp	Phe	Thr	Glu	Asn	Pro	Cys	Leu	Arg	Asn	Ala	
	370					375					380					
Ile	Gln	Ala	Phe	Gly	Asn	Gly	Thr	Asp	Val	Asn	Met	Ser	Pro	Lys	Gly	
385					390					395					400	
Pro	Ser	Leu	Pro	Ala	Thr	Gln	Ala	Pro	Arg	Val	Glu	Lys	Thr	Pro	Ser	
				405					410					415		
Leu	Pro	Asp	Asp	Leu	Ser	Asp	Ser	Thr	Ser	Leu	Gly	Thr	Ser	Val	Ile	
			420					425					430			
Thr	Thr	Cys	Thr	Ser	Ile	Gln	Glu	Gln	Gly	Leu	Lys	Ala	Asn	Asn	Ser	
		435					440					445				
Lys	Glu	Leu	Ser	Met	Cys	Phe	Thr	Glu	Leu	Thr	Thr	Asn	Ile	Ile	Pro	
	450					455					460					
Gly	Trp	Arg	Ala	Trp	Val	Pro	Val	Val	Leu	Gly	Val	Leu	Thr	Ala	Leu	
465					470					475					480	
Val	Thr	Ala	Ala	Ala	Leu	Ala	Leu	Ile	Leu	Leu	Arg	Lys	Arg	Arg	Lys	
				485					490					495		
Glu	Thr	Arg	Phe	Gly	Gln	Ala	Phe	Asp	Ser	Val	Met	Ala	Arg	Gly	Glu	
		500						505					510			
Pro	Ala	Val	His	Phe	Arg	Ala	Ala	Arg	Ser	Phe	Asn	Arg	Glu	Arg	Pro	
		515					520					525				
Glu	Arg	Ile	Glu	Ala	Thr	Leu	Asp	Ser	Leu	Gly	Ile	Ser	Asp	Glu	Leu	
	530					535					540					
Lys	Glu	Lys	Leu	Glu	Asp	Val	Leu	Ile	Pro	Glu	Gln	Gln	Phe	Thr	Leu	
545					550					555					560	
Gly	Arg	Met	Leu	Gly	Lys	Gly	Glu	Phe	Gly	Ser	Val	Arg	Glu	Ala	Gln	
				565					570					575		
Leu	Lys	Gln	Glu	Asp	Gly	Ser	Phe	Val	Lys	Val	Ala	Val	Lys	Met	Leu	
			580					585					590			
Lys	Ala	Asp	Ile	Ile	Ala	Ser	Ser	Asp	Ile	Glu	Glu	Phe	Leu	Arg	Glu	
		595					600					605				
Ala	Ala	Cys	Met	Lys	Glu	Phe	Asp	His	Pro	His	Val	Ala	Lys	Leu	Val	
	610					615					620					
Gly	Val	Ser	Leu	Arg	Ser	Arg	Ala	Lys	Gly	Arg	Leu	Pro	Ile	Pro	Met	
625					630					635					640	
Val	Ile	Leu	Pro	Phe	Met	Lys	His	Gly	Asp	Leu	His	Ala	Phe	Leu	Leu	
				645					650					655		
Ala	Ser	Arg	Ile	Gly	Glu	Asn	Pro	Phe	Asn	Leu	Pro	Leu	Gln	Thr	Leu	
			660					665					670			
Ile	Arg	Phe	Met	Val	Asp	Ile	Ala	Cys	Gly	Met	Glu	Tyr	Leu	Ser	Ser	
		675					680					685				
Arg	Asn	Phe	Ile	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Cys	Met	Leu	Ala	
	690					695				700						
Glu	Asp	Met	Thr	Val	Cys	Val	Ala	Asp	Phe	Gly	Leu	Ser	Arg	Lys	Ile	
705					710				715						720	
Tyr	Ser	Gly	Asp	Tyr	Tyr	Arg	Gln	Gly	Cys	Ala	Ser	Lys	Leu	Pro	Val	

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<211> 888
<212> PRT
<213> Artificial Sequence
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<220>
<223> Chimeric receptor comprising murine sequence.

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Ser Leu Lys Met Ala Asp Pro Asn Arg Phe Arg Gly Lys Asp Leu Pro
      35             40             45
Val Leu Asp Gln Leu Leu Glu Ala Gly Asn Ser Leu Ala Thr Glu Asn
      50             55             60
Arg Phe Val Asn Ser Cys Thr Gln Ala Arg Lys Lys Cys Glu Ala Asn
65             70             75             80
Pro Ala Cys Lys Ala Ala Tyr Gln His Leu Gly Ser Cys Thr Ser Ser
      85             90             95
Leu Ser Arg Pro Leu Pro Leu Glu Glu Ser Ala Met Ser Ala Asp Cys
      100            105            110
Leu Glu Ala Ala Glu Gln Leu Arg Asn Ser Ser Leu Ile Asp Cys Arg
      115            120            125
Cys His Arg Arg Met Lys His Gln Ala Thr Cys Leu Asp Ile Tyr Trp

```


E3

130	135	140
Thr Val His Pro Ala Arg	Ser Leu Gly Asp Tyr	Glu Leu Asp Val Ser
145	150	155
Pro Tyr Glu Asp Thr Val	Thr Ser Lys Pro Trp	Lys Met Asn Leu Ser
165	170	175
Lys Leu Asn Met Leu Lys	Pro Asp Ser Asp Leu	Cys Leu Lys Phe Ala
180	185	190
Met Leu Cys Thr Leu His	Asp Lys Cys Asp Arg	Leu Arg Lys Ala Tyr
195	200	205
Gly Glu Ala Cys Ser Gly	Ile Arg Cys Gln Arg	His Leu Cys Leu Ala
210	215	220
Gln Leu Arg Ser Phe Phe	Glu Lys Ala Ala Glu	Ser His Ala Gln Gly
225	230	235
Leu Leu Leu Cys Pro Cys	Pro Pro Glu Asp Ala	Gly Cys Gly Glu Arg
245	250	255
Arg Arg Asn Thr Ile Ala	Pro Ser Cys Ala Leu	Pro Ser Val Thr Pro
260	265	270
Asn Cys Leu Asp Leu Arg	Ser Phe Cys Arg Ala	Asp Pro Leu Cys Arg
275	280	285
Ser Arg Leu Met Asp Phe	Gln Thr His Cys His	Pro Met Asp Ile Leu
290	295	300
Gly Thr Cys Ala Thr Glu	Gln Ser Arg Cys Leu	Arg Ala Tyr Leu Gly
305	310	315
Leu Ile Gly Thr Ala Met	Thr Pro Asn Phe Ile	Ser Lys Val Asn Thr
325	330	335
Thr Val Ala Leu Ser Cys	Thr Cys Arg Gly Ser	Gly Asn Leu Gln Asp
340	345	350
Glu Cys Glu Gln Leu Glu	Arg Ser Phe Ser Gln	Asn Pro Cys Leu Val
355	360	365
Glu Ala Ile Ala Ala Lys	Met Arg Phe His Arg	Gln Leu Phe Ser Gln
370	375	380
Asp Trp Ala Asp Ser Thr	Phe Ser Val Val Gln	Gln Gln Asn Ser Asn
385	390	395
Pro Ala Trp Arg Ala Trp	Val Pro Val Val Leu	Gly Val Leu Thr Ala
405	410	415
Leu Val Thr Ala Ala Ala	Leu Ala Leu Ile Leu	Leu Arg Lys Arg Arg
420	425	430
Lys Glu Thr Arg Phe Gly	Gln Ala Phe Asp Ser	Val Met Ala Arg Gly
435	440	445
Glu Pro Ala Val His Phe	Arg Ala Ala Arg Ser	Phe Asn Arg Glu Arg
450	455	460
Pro Glu Arg Ile Glu Ala	Thr Leu Asp Ser Leu	Gly Ile Ser Asp Glu
465	470	475
Leu Lys Glu Lys Leu Glu	Asp Val Leu Ile Pro	Glu Gln Gln Phe Thr
485	490	495
Leu Gly Arg Met Leu Gly	Lys Gly Glu Phe Gly	Ser Val Arg Glu Ala
500	505	510
Gln Leu Lys Gln Glu Asp	Gly Ser Phe Val Lys	Val Ala Val Lys Met
515	520	525
Leu Lys Ala Asp Ile Ile	Ala Ser Ser Asp Ile	Glu Glu Phe Leu Arg
530	535	540
Glu Ala Ala Cys Met Lys	Glu Phe Asp His Pro	His Val Ala Lys Leu
545	550	555
Val Gly Val Ser Leu Arg	Ser Arg Ala Lys Gly	Arg Leu Pro Ile Pro
565	570	575
Met Val Ile Leu Pro Phe	Met Lys His Gly Asp	Leu His Ala Phe Leu
580	585	590

E3

Leu	Ala	Ser	Arg	Ile	Gly	Glu	Asn	Pro	Phe	Asn	Leu	Pro	Leu	Gln	Thr
		595					600					605			
Leu	Ile	Arg	Phe	Met	Val	Asp	Ile	Ala	Cys	Gly	Met	Glu	Tyr	Leu	Ser
	610					615					620				
Ser	Arg	Asn	Phe	Ile	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Cys	Met	Leu
625					630					635					640
Ala	Glu	Asp	Met	Thr	Val	Cys	Val	Ala	Asp	Phe	Gly	Leu	Ser	Arg	Lys
			645						650					655	
Ile	Tyr	Ser	Gly	Asp	Tyr	Tyr	Arg	Gln	Gly	Cys	Ala	Ser	Lys	Leu	Pro
		660						665					670		
Val	Lys	Trp	Leu	Ala	Leu	Glu	Ser	Leu	Ala	Asp	Asn	Leu	Tyr	Thr	Val
	675						680					685			
Gln	Ser	Asp	Val	Trp	Ala	Phe	Gly	Val	Thr	Met	Trp	Glu	Ile	Met	Thr
	690					695					700				
Arg	Gly	Gln	Thr	Pro	Tyr	Ala	Gly	Ile	Glu	Asn	Ala	Glu	Ile	Tyr	Asn
705					710					715					720
Tyr	Leu	Ile	Gly	Gly	Asn	Arg	Leu	Lys	Gln	Pro	Pro	Glu	Cys	Met	Glu
			725						730					735	
Asp	Val	Tyr	Asp	Leu	Met	Tyr	Gln	Cys	Trp	Ser	Ala	Asp	Pro	Lys	Gln
			740					745				750			
Arg	Pro	Ser	Phe	Thr	Cys	Leu	Arg	Met	Glu	Leu	Glu	Asn	Ile	Leu	Gly
		755					760					765			
Gln	Leu	Ser	Val	Leu	Ser	Ala	Ser	Gln	Asp	Pro	Leu	Tyr	Ile	Asn	Ile
	770					775					780				
Glu	Arg	Ala	Glu	Glu	Pro	Thr	Ala	Gly	Gly	Ser	Leu	Glu	Leu	Pro	Gly
785					790					795					800
Arg	Asp	Gln	Pro	Tyr	Ser	Gly	Ala	Gly	Asp	Gly	Ser	Gly	Met	Gly	Ala
			805						810					815	
Val	Gly	Gly	Thr	Pro	Ser	Asp	Cys	Arg	Tyr	Ile	Leu	Thr	Pro	Gly	Gly
		820						825					830		
Leu	Ala	Glu	Gln	Pro	Gly	Gln	Ala	Glu	His	Gln	Pro	Glu	Ser	Pro	Leu
		835					840					845			
Asn	Glu	Thr	Gln	Arg	Leu	Leu	Leu	Leu	Gln	Gln	Gly	Leu	Leu	Pro	His
	850					855					860				
Ser	Ser	Cys	Ala	Asp	Ala	Ser	Leu	Lys	Met	Ala	Asp	Pro	Asn	Arg	Phe
865					870					875					880
Arg	Gly	Lys	Asp	Leu	Pro	Val	Leu								
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37

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20

<210> 23

E3

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